



ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC 60
ATGTGCTTTT TAAATTGGCC TGGGTGACCC GCCCACTTGG TGTAAGAAGAA GAACCGGCCA 120
AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC 180
TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35 40
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50 55
GGA GCT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65 70

FIG. 1A



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ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt	471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu	
75 80 85	
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG	519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu	
90 95 100 105	
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110 115 120	
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125 130 135	
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT	663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn	
140 145 150	
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155 160 165	

FIG. 1B



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TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG	759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln	185
170 175 180	
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT	807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly	200
190 195	
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	215
205 210	
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	230
220 225	
TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	245
235 240	
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	265
250 255	

FIG. 1C



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ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	270 275 280
TTT GGG GGT GTG AAA TAC CAG TAT GGT AAC CAA GAA GGG GAG ATG	1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Asn Gln Glu Gly Glu Met	285 290 295
GGC TTT GAA CCC TGC TAT TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA	1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	300 305 310
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	315 320 325
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC CAC TTG ATC GAT TAT GAA AAG	1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	330 335 340 345
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG	1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	350 355 360

FIG. 1D



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TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG	1335
Cys Asp Asn Leu Gly Ser Phe Ser Gly Ser Pro Phe Leu Cys Met	375
	365
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala	390
	385
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC	1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp	405
	395
	400
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT	1479
Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His	425
	415
	420
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA	1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro	440
	430
	435
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT	1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser	455
	445
	450

FIG. 1E



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GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT 1629
Gly Lys Ala Trp Pro Glu Thr Arg
460 465

TAGATGAGTC TTGCTCTTGA GCCTAGTGAT TTGGGCTTCA ATGATTTGCA CATCTAATGT 1689

GAATAGCTCC TAACCACTTG GTGGGTGCAT GGCTGGCACC AGACTGTAAA TCTTTTGGGA 1749

TTCTTTGTAC AGAGTCCTGC AAAGGAAAAA AGAGAAAAGG TTTGGAACTC CATGCTAGAT 1809

TGCGAGTTCA GAGACAGGTC CCTGGGGACC AAAGAACAAT CTCGTTTCAA CCCTTGGATG 1869

CCTCATTTGCT TTGAATGGAT TCATTTTTCG TTATAAGCTG ATTACTGAA ATCCCATAAC 1929

CCATCAATGC TGTTAATTTT TTTCTTCCTA CCCTTATTAC ATTCCCTACC CTAAAAGCCT 1989

GGGGGAAATA CCTGGTTTTG CTTCCCATCT ATAATTGAGA AAGAGGGGGG AAAAGATACT 2049

GTATTAGAAAT TTGTGTGATC CTGTGGCACA ATAGATCAAC CAACCCATTT AAAGCTTAAA 2109

AAAAAAAAAA 2119

FIG. 1F



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peaNTase 1	1	-----MELLIKLTFLFSMPAITSQYLGNNLLTSRKIFLKQEEISSYAVVFDAGSTGSR
potapyrase 1	1	MLNQNSHFIFIIAIFLVLP LSLSKNVNAQIP LRRHLLSHESE--HYAVIFDAGSTGSR
mNTase 1	1	MATSWGAVFPM LIIACVGVSTVFYREQQTWFEQVFLSSMCPINVSAGTFY GIMFDAGSTGTR
YGDase 1	1	KTPEDISILPVNDEPGYLQDSKTEQNYPELADAVKTSQTSCTSEHKYVIMIDAGSTGSR
peaNTase 57	57	IHVYHFNQNLDLLHIGKGVVEYNNKITPGLSSYANNPEQA AKSLIP LLEQAEDVVPDDLQP
potapyrase 59	59	VHVFRFDEKLG LLLPIGN NIEYFMATEPGLSSYAE DPKAAANSLEPLLDGAEGVVPQELQS
mNTase 61	61	IHVYTFVQKTAGQLPFLGEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSHWE
YGDase 61	61	VHIYKFDVCTS--PPTLLDEKFDMLEPGLSSFDTDSVGAAANSLDPLKKVAMNYVPIKARS
peaNTase 117	117	KTPVRLGATAGLRLLLNGDASEKILQSVRDMLSNRSTF-NVQPD AVSII DGTQEGSYLWVT
potapyrase 119	119	ETPLELGATAGLRMLKGDAAEKILQAVRNLVKNQSTF-HSKDQWVTILDGTQEGSYMWAA
mNTase 121	121	RTPVVLKATAGLRLLP EQKAQALLLEVEEIEFKN-SPF-LVPDGSV SIMDGSYEGILAWVT
YGDase 119	119	CTPVAVKATAGLRLLLGDAXSSKILSAVRDHLEKDYPPFPVVEGDGV SIMGDEEGVFAWIT

FIG. 2A

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peaNTase	176	VNYALGNLGGKYYTK--TVGVIDLGGGSVQMAYAVSKKTAKNAPKVADGDDPYIKKVVVLKG
potapyrase	178	INYLGNLGGKDYKS--TTATIDLGGGSVQMAYAISNEQFAKAPQNEG-EPYVQXHLMS
mNTase	179	VNFLTQQLHGRGQE--TVGTLDLGGASTQITFLPQFEK-----TLEQTPRGYLTSEMFN
YGDPase	179	TNYLLGNIGANGPKLPPTAAVFDLGGGSTQIVFEP--TFPINEKMOVGEHKF--DLKFGD
peaNTase	234	IPYDLVYVHSYLVHFGREASRAEILKL-----TPRSPNPCLLAGFNGIY
potapyrase	235	KDYNLYVHSYLVNYGQLAGRAEIPKA-----SRNESNPCALEGCDGY
mNTase	232	STFKLYTHSYLVGFGGLKAARLATLGA-----LEAKGT--DGHTFRS
YGDPase	234	ENYTLVYQFVSHLVGYGLKEGRNKNVNSVLVENALKDGKILKGDNTKTHQLSSPCLPPKVNATN
peaNTase	276	TYSGEEFKATAYTSGA-----NFNKCKNTIRKALKLNYPQNYQNTFGGIWNGGGN---
potapyrase	277	SYGGVDYKVKAPKKGS-----SWKRCRRLLTRHALKINAKCNIEECTFNGVWNGGGD---
mNTase	270	ACLPRWLEAEWIFGGV-----KYQYGGNQEGEMGFEPFCYAEVLRVVQGLHQPEEVR---
YGDPase	294	EKVTLESKEITYTIDFVIGPDEPSGAQCRFLTDEILNKDAQCQSPPCSFNGVHQPSLVRTFK

FIG. 2B



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peaNTase 328 GQKNLPASSFFYLPEDTGMVDASTPNFILLRPVDIETKAKEACALNFEDAKSTYPLDKK
potapyrase 329 GQKNIHASSFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKSIFPKTQDR
mNTase 322 GSA-FYAPSYYDRAADTHLIDYE-KGGVLKVEDFERKAREVCD-NLGSFSSGGSP-----
YGDase 354 ESNDIYIFSYFYDRTRPLGMPLSFTLNELDLARIIVCKGEETWNSVPSGIAGS-----LDEL

peaNTase 388 NVASYVCMDLIYQVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVEAISALPK
potapyrase 389 NI-PYLCMDLIYEYTLLVGGFGLNPHKEITVIHDVQYKNYLVGAAWPLGCAIDLVSSTTN
mNTase 374 -----FLCMDLTYITALLKDGLGFAERHPLTAHKESEQHRDWLGLGHLSPAPVSGHHQLR
YGDase 411 ESDSHFCLDLSFQVSLLHTGYDIPLORELRTGKKIANKE-----IGWCLGASLPLLLKADNW

peaNTase 448 FERLMYFV
potapyrase 448 KIRVASS*
mNTase 430 PSSTSEACISEPVFSQEGVDSETFSDLSGKAWPETR*
YGDase 467 KCKIQSA

FIG. 2C



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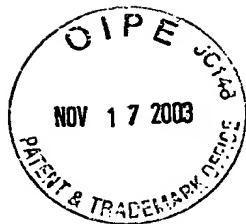
		ACRI	
CD39	1	VKYGIVLDAGSSHTS	LYIYKW-----PAEKENDTGV-----VHQVEECRVK-GPGIS
ratCD39	1	VKYGIVLDAGSSHTN	LYIYKW-----PAEKENDTGV-----VQLLEECQVK-GPGIS
CD39L1	1	LKYGIVLDAGSSHTS	MFIYKW-----PADKENDTGI-----VGQHSSCDVP-GGGIS
chiATPase	1	FKYGIVLDAGSSHTA	VFIYKW-----PADKENDTGV-----VSEHSMCDVE-GPGIS
peanTPase	1	SSYAVVFDAGSTGSR	IHVYHF-----NQ-NLDLLHIGKGV EY N-----KITPGLS
potRROP1	1	EHYAVIFDAGSTGSR	VHVFRF-----DE-KLGLLPIGN NIEYFM-----ATEPGLS
YGDA1	1	HKYVIMIDAGSTGSR	VHIYKF-----DVCTSP--PTLLD-EKFD-----MLEPGLS
mNTase	1	TFYGIMFDAGSTGTR	IHVYTF-----VQKTAGQLPFL EG-EIFD-----SVKPGLS
hCD39L2	1	-----	-----FK-----ALKPGLS
celegans	1	IKYGVICDAGSSGTR	LFVYTLKPLSGGL--TNIDT--L-----IHSEPVVKKVT PGLS
y71KD	1	DRFGIVIDAGSSGSR	IHVFKWQDTESSLHATNQDSQSILQSVPHIHQEKDWTFKLNPGLS

FIG. 3A



		ACR II			
CD39	47	K <u>F</u> -VQK <u>V</u> NEIGI-YLTDCMERAREV <u>I</u> PR--S-QHQETPVYLGATAGMRLLRMES <u>E</u> ELAD			
ratCD39	47	KY-AQKTDEIAA-YLAECMKMSTERIPA--SKHQ-TPVYLGATAGMRLLRMESKQ <u>S</u> AD			
CD39L1	47	SY-ADNP <u>S</u> GASQ-SLVGCLEQA <u>L</u> QDVPK--ER-HAGTPLYLGATAGMRLLNLTNPEAST			
chiATPase	47	SY-SSKPPAAGK-SLEHCLSQAMRDVPK--EK-HADTPLYLGATAGMRLLTIADPPSQT			
peaNTPase	46	SY-ANNPEQA <u>A</u> KS-LIPLLEQAEDVVP--DDLQPKTPVRLGATAGLRLLN--GDA-SE			
potRROPI	46	SY-AEDPKAAANS-LEPLLDGAE <u>G</u> VVP--QELQSETPLELGATAGLRMLK--GDA-AE			
YGDA1	44	SFDTSV-GAANS-LDPLLLKVAMNVVPI--KARSCTPVAVKATAGLRLL--GDAKSS			
mNTPase	46	AF-VDQPKQGAET-VQELLEVAKDSIPRSHWE--R--TPVVLKATAGLRLL--PEQKAQ			
hCD39L2	10	AY-ADDVEKSAQG-IRELLDVAKQDIP--FDSGRP-TPLVLKATAGLRLL--PGEKAQ			
celegans	51	SFG-DKPEQVVE-YLTPLLRFAEEHIPPYEQLGE--TDLLIFFATAGMRLL--PEAQKD			
Y71KD	61	SFE-KKPPQDAYKSHIKPLLLDFAKNIIPESHWSS--CPVFIQATAGMRLL--PQDIQS			

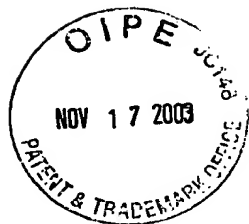
FIG. 3B



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		ACR III																																																								
CD39	101	RVL	DV	VER	SL	N	-	Y	P	F	-	-	-	-	-	D	F	Q	G	A	R	I	I	T	G	Q	E	E	G	A	Y	G	W	I	T	I	N	Y	L	L	G	K	F	S	Q	K	T	R	W	F	S	I	V	P				
ratCD39	101	EVL	AA	V	S	R	S	L	K	S	-	Y	P	F	-	-	-	-	D	F	Q	G	A	K	I	I	T	G	Q	E	E	G	A	Y	G	W	I	T	I	N	Y	L	L	G	R	F	T	Q	E	Q	S	W	L	N	F	I	S	
CD39L1	101	SVL	MA	V	T	H	T	L	T	Q	-	Y	P	F	-	-	-	-	D	F	R	G	A	R	I	L	S	G	Q	E	E	G	V	F	G	W	V	T	A	N	Y	L	L	E	N	F	I	-	K	Y	G	W	V	G	-	-	R	
chiATPase	101	-	CL	SA	V	M	A	T	L	K	S	-	Y	P	F	-	-	-	-	D	F	G	G	A	K	I	L	S	G	E	E	E	G	V	F	G	W	I	T	A	N	Y	L	L	E	N	F	I	-	K	R	G	W	L	G	-	-	E
peaNTase	97	KIL	Q	S	V	R	D	M	L	S	N	R	S	T	F	N	-	V	Q	P	D	-	A	-	V	S	I	I	D	G	T	Q	E	G	S	Y	L	W	V	T	V	N	Y	A	L	G	N	-	-	-	-	-	L	-	-	-	G	
potRROP1	97	KIL	Q	A	V	R	N	L	V	K	N	Q	S	T	F	H	-	-	S	K	D	-	Q	W	V	T	I	L	D	G	T	Q	E	G	S	Y	M	W	A	A	I	N	Y	L	L	G	N	-	-	-	-	-	L	-	-	-	G	
yGDA1	95	KIL	SA	V	R	D	H	L	E	K	D	Y	P	P	P	V	E	G	D	-	G	-	V	S	I	M	G	G	D	E	E	G	V	F	A	W	I	T	T	N	Y	L	L	G	N	-	-	-	-	-	I	G	A	N	G			
mNTase	97	ALL	L	E	V	E	E	I	F	-	K	N	S	P	F	-	L	V	-	P	D	-	G	S	V	S	I	M	D	G	S	Y	E	G	I	L	A	W	V	T	V	N	F	L	T	G	Q	-	-	-	-	-	L	H	G	R	G	
hCD39L2	61	KLL	Q	K	V	K	E	Y	L	-	K	H	S	P	F	-	L	V	-	G	D	-	D	C	V	S	I	M	N	G	T	D	E	G	V	S	A	W	X	T	I	N	F	L	T	G	S	-	-	-	-	-	L	K	T	P	G	
celegans	102	AII	K	N	L	Q	N	G	L	K	S	V	T	A	L	R	V	S	D	-	-	-	S	N	I	R	I	I	D	G	A	W	E	G	I	Y	S	W	I	A	V	N	Y	I	L	G	R	-	-	-	-	-	F	-	D	-	-	
y1KD	113	SIL	D	G	L	C	Q	G	L	K	H	P	A	E	F	L	V	E	D	C	S	-	A	Q	I	Q	V	I	D	G	E	T	E	G	L	Y	G	W	L	G	L	N	Y	L	Y	G	H	-	-	-	-	-	F	N	D	Y	N	

FIG. 3C



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ACR IV			
CD39	155	<u>Y</u> <u>E</u> <u>T</u> <u>N</u> <u>N</u> <u>Q</u> <u>E</u> <u>T</u> <u>F</u> <u>G</u> <u>A</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>V</u> <u>T</u> <u>F</u> <u>V</u> <u>P</u> <u>Q</u> <u>N</u> <u>Q</u>	
ratCD39	155	- <u>D</u> <u>S</u> <u>Q</u> <u>K</u> <u>Q</u> <u>A</u> <u>T</u> <u>F</u> <u>G</u> <u>A</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>S</u> <u>T</u> <u>Q</u> <u>V</u> <u>T</u> <u>F</u> <u>V</u> <u>P</u> <u>L</u> <u>N</u> <u>Q</u>	
CD39L1	152	<u>W</u> <u>F</u> <u>R</u> <u>P</u> <u>R</u> <u>K</u> <u>G</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> <u>M</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>E</u> <u>T</u> <u>T</u> <u>S</u> <u>P</u>	
chiATPase	151	<u>W</u> <u>I</u> <u>Q</u> <u>S</u> <u>K</u> <u>K</u> <u>K</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> <u>M</u> <u>D</u> <u>F</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>E</u> <u>T</u> <u>S</u> <u>D</u> <u>A</u> <u>I</u>	
peaNTPase	144	<u>K</u> <u>K</u> <u>Y</u> <u>T</u> <u>K</u> - - <u>T</u> <u>V</u> <u>G</u> <u>V</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>V</u> <u>S</u> <u>K</u> <u>K</u>	
potRROP1	144	<u>K</u> <u>D</u> <u>Y</u> <u>K</u> <u>S</u> - - <u>T</u> <u>T</u> <u>A</u> <u>T</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>I</u> <u>S</u> <u>N</u> <u>E</u>	
YGDA1	146	<u>P</u> <u>K</u> <u>L</u> - <u>P</u> - - <u>T</u> <u>A</u> <u>A</u> <u>V</u> <u>F</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>V</u> <u>F</u> <u>E</u> <u>P</u> <u>T</u> <u>F</u> <u>P</u> <u>I</u>	
mNTPase	146	<u>Q</u> <u>E</u> - - - - - <u>T</u> <u>V</u> <u>G</u> <u>T</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>L</u> <u>P</u> <u>Q</u> <u>F</u> <u>E</u>	
hCD39L2	110	<u>G</u> <u>S</u> - - - - - <u>S</u> <u>V</u> <u>G</u> <u>M</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>A</u> <u>F</u> <u>L</u> <u>P</u> <u>R</u> <u>V</u> <u>E</u>	
celegans	149	<u>K</u> <u>E</u> - <u>N</u> <u>D</u> <u>S</u> - <u>K</u> <u>V</u> <u>G</u> <u>M</u> <u>I</u> <u>D</u> <u>M</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>V</u> <u>Q</u> <u>I</u> <u>A</u> <u>F</u> <u>E</u> <u>I</u> <u>A</u> - <u>N</u> <u>E</u>	
y71KD	165	<u>P</u> <u>E</u> <u>V</u> <u>S</u> <u>D</u> <u>H</u> <u>F</u> <u>T</u> <u>F</u> <u>G</u> <u>F</u> <u>M</u> <u>D</u> <u>M</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>A</u> <u>F</u> - - <u>A</u> <u>P</u> <u>H</u> <u>D</u> <u>S</u>	

FIG. 3D



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GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCCAA 60
AAGACCGGCT GCCGCCTGCT CCCCAGGAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC 120
GCGCGGTGCA TGGATGGC TATGTGAATG AAAAAAGTA TCCGTTATGA AACTTCCAGA 180
AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GGCAACAAG G ATG AGA 237
Met Arg
1
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC 285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
5 10 15
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG 333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
20 25 30
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC 381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
35 40 45 50

FIG. 4A



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CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT Pro Gly Ala Arg Trp Gly Gln Ala His Ser Pro Leu Gly Thr Ala	429
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC Ala Asp Gly His Gln Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	477
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	525
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	573
100 105 110	
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	621
115 120 125 130	

FIG. 4B



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CTA CTG GAT GTT GCT AAA CAG GAC GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	145
	140
	135
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	160
	155
	150
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	175
	170
	165
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	190
	185
	180
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	210
	200
	195
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	225
	215
	220

FIG. 4C



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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG	957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln	230 235 240
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC	1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr	245 250 255
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA	1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Met Ser Ala	260 265 270
CGC CTG GCG ATC CTG GGC GGC GAG GAG GGC CCT GCT AAG GAT GGA	1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly	275 280 285 290
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG	1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp	295 300 305
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA	1197
Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala	310 315 320

FIG. 4D



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AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC	1245
Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn	
325 330 335	
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC	1293
Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe	
340 345 350	
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG	1341
Ser Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu	
355 360 365 370	
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC	1389
Lys Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr	
375 380 385	
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC	1437
Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys	
390 395 400	
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC	1485
Met Asp Leu Thr Tyr Val Ser Leu Leu Gln Glu Phe Gly Phe Pro	
405 410 415	

FIG. 4E



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AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC 1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
420 425 430

AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA 1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
435 440 445 450

CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG 1629
Gln Lys Ser Pro Ala Ser
455

CAGTGTCTGT GTGTCTGCAAT AAACCCCTCCT GTCCCTGGACG TGA CTTTCATC CTGAGGAGGCC 1689

ACAGCACAGG CCGTGCTGGC ACTTTCIGCA CACTGGCTCT GGGACTTGCA GAAGGCCCTGG 1749

TGCTGCCCTG GCATCAGCCT CTTCCAGTCA CATCTGGCCA GAGGGCTGTC TGGACCTGGG 1809

CCCTGTCTAA TGCCACCTGT CTGCCTGGGC TCCAAGTGGG CAGGACCAGG ACAGAACCAC 1869

AGGCACACAC TGAGGGGGCA GTGTGGCTCC CTGCCCTGTCC CATCCCCATG CCCCCGTCCG 1929

FIG. 4F



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GGGGCTGTGG CTGCTGCTGT GCATGTCCCT GCGATGGGAG TCTTGTCTCC CAGCCTGTCA 1989
GTTTCCCTCCC CAGGGCAGAG CTCCCCCTTC TCAAGAGTC TGGAGGCGG TGCAGGCTGT 2049
CCTGGCTGCT CTGGGGAAGC CGAGGGACAG CCATAACACC CCCGGGACAG TAGGTCTGGG 2109
CGGCACCACT GGGAACTCTG GACTTGAGTG TGTGTGCTCT TCCTTGGGTA TGAATGTGTG 2169
AGTTCACCCA GAGGCCCTGCT CTCCTCACAC ATTGTGTGGT TTGGGGTTAA TGATGGAGGG 2229
AGACACCTCT TCATAGACGG CAGGTGCCCCA CCTTTCAGG AGTCTCCCAG CATGGGCGGA 2289
TGCCGGGCAT GAGCTGCTGT AAACATATTG TGGCTGTGCT GCTTGAGTGA CGTCTCTGTC 2349
GTGTGGGTGC CAAGTGCTTG TGTAGAACT GTGTTCTGAG CCCCCCTTTC TGGACACCAA 2409
CTGTGTCCTG TGAATGTATC GCTACTGTGA GCTGTTCCCC CCTAGCCAGG GCCATGTCTT 2469
AGGTGCAGCT GTGCCACGG TCAGCTGAGC CACAGTCCCA GAACCAAGCT CTCGGTGTCT 2529

FIG. 4G



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CGGGCCACCA TCGGGCCACC TCGGGCTGAC CCCACCTCCT CCATGGACAG TGTGAGCCCC 2589
GGCCCGTGCA TCCTGCTCAG TGTGGCGTCA GTGTCGGGGC TGAGCCCCCTT GAGCTGCTTC 2649
AGTGAATGTA CAGTGCCCGG CACGAGCTGA ACCTCATGTG TTCCACTCCC AATAAAAGGT 2709
TGACAGGGGC TTCTCCTTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 2762

FIG. 4H



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FIG. 5A

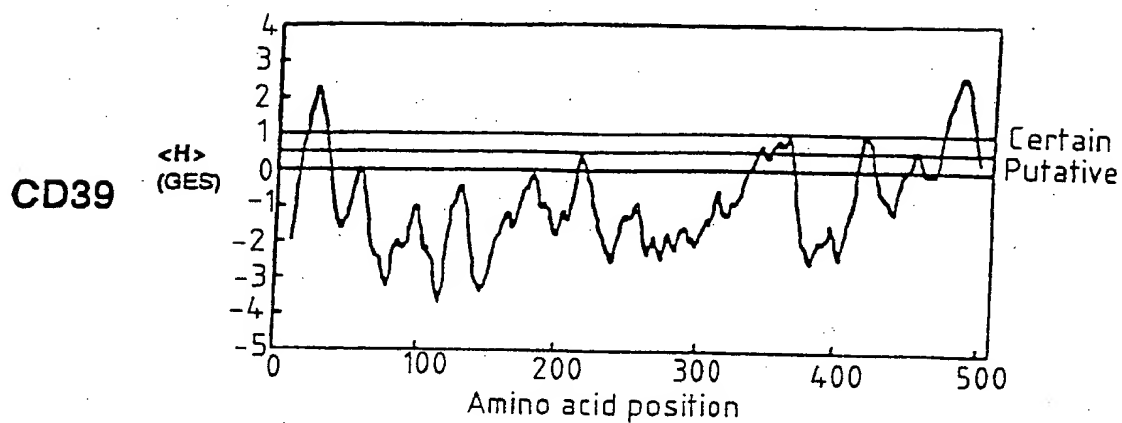


FIG. 5B

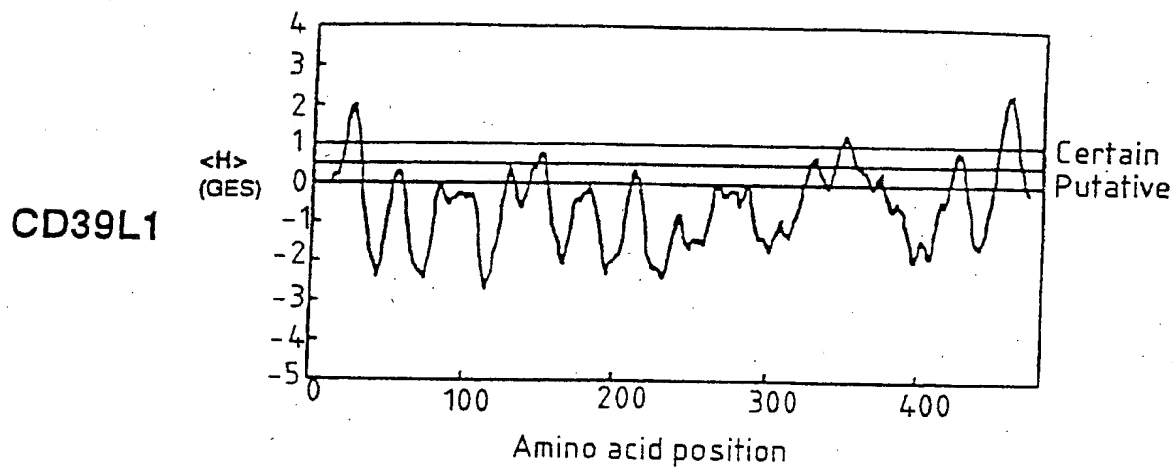
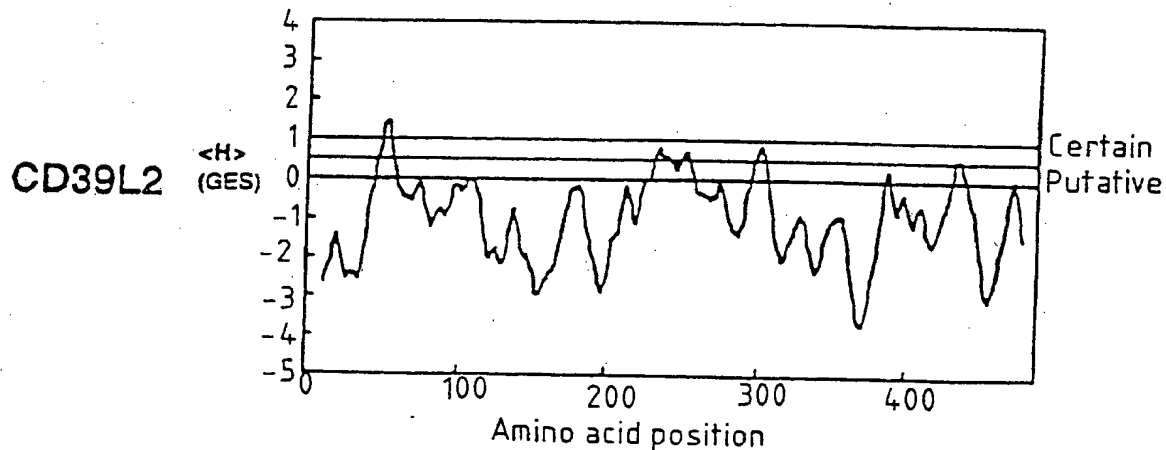


FIG. 5C





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FIG. 5D

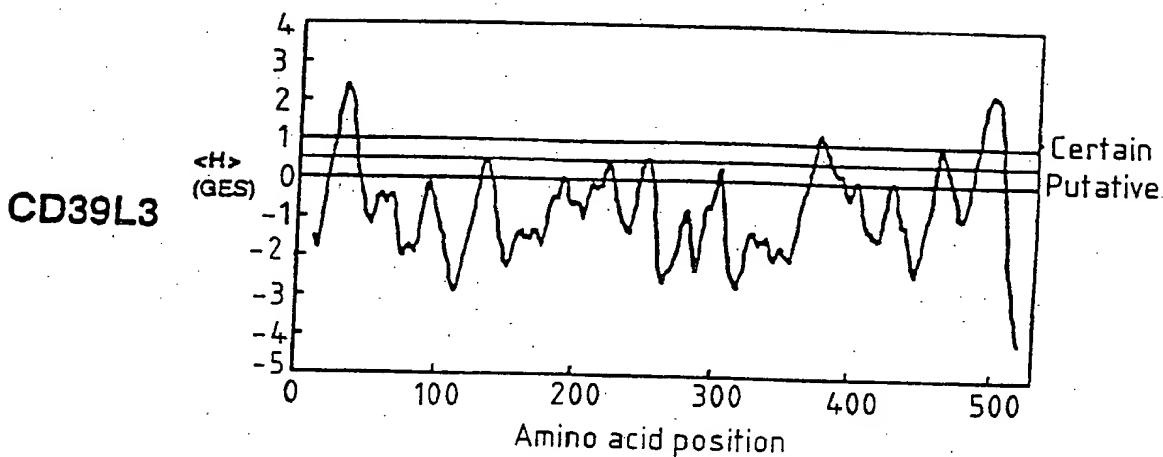
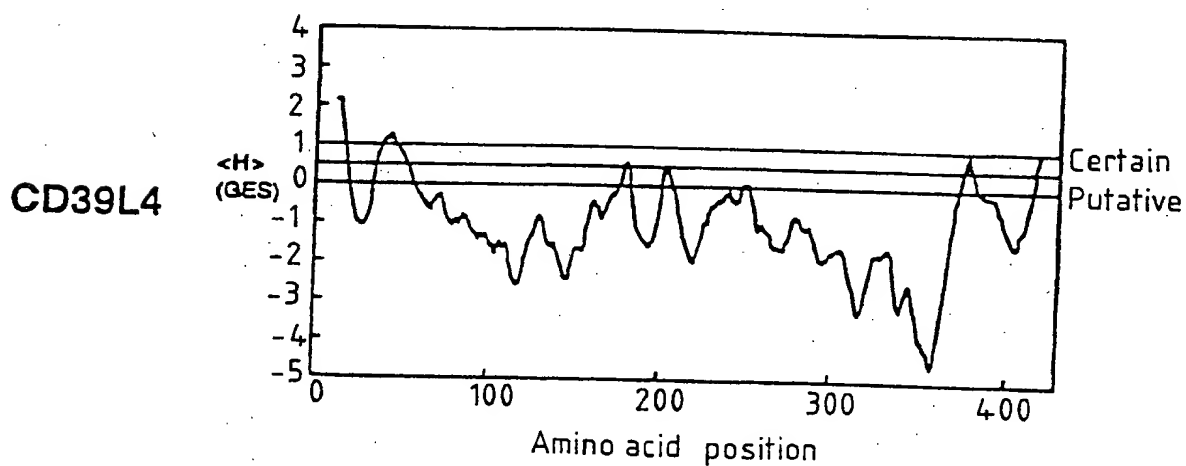
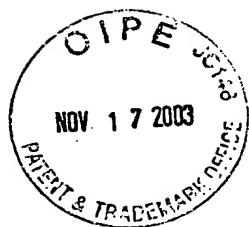


FIG. 5E





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ACCCACGGGT CTGGCCGGG GCGCCTCTG CGCAGCGCT AGTCGCCTTC TCCGAATCGG 60
CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT 112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys 10
1 5
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC 160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala 25
15 20
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC 208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val 40
30 35
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT 256
Ile Gln Ile His Lys Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly 50
45 55
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA 304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln 60
65 70

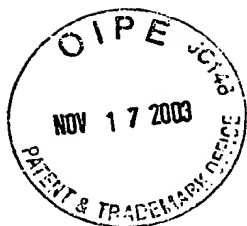
FIG. 6A



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TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Thr Gly Val Ser Gln Thr Phe	90
75 80 85	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	105
95 100	
caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	120
110 115	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	135
125 130	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Arg Leu Gln Asn Glu Thr Ala Ala Asn	150
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	170
155 160 165	

FIG. 6B



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TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Gly Val Tyr Gly	185
	175
	180
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	200
	190
	195
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	210
	205
	215
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	230
	220
	225
ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	240
	235
	245
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	255
	260
	265



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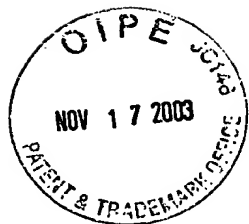
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	
270 275 280	
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC	976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	
285 290 295	
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	
300 305 310	
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	
315 320 325 330	
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	
350 355 360	



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ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC TAC ACA GCC AGT	1216
Ile Lys Gly Pro Phe Val Ala Phe 370	
365	
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC	1264
Ala Leu Asn Leu Ser Gly Ser Phe 385	
380	
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC	1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu 410	
395	
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC	1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 425	
415	
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT	1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 440	
430	
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC	1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 455	
445	

FIG. 6E



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TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA 1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu
460 465 470

AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC 1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr
475 480 485 490

CTC GCT TTC TCA GCA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA 1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala
495 500 505

TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT 1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe
510 515 520

GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA 1699
Asp His Ala Val Asp Ser Asp
525

TGGCTGCTTA GAGTCAGCCT GGGTGGCACC AGGCAATGCA GGTGAAGTGG CTGCCTTCAG 1759



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GAAATACAAC TAACTAAAT CAAACACCTA GGTACAGTGC CTCTCAAATA CTGATTCTTG 1819
CCACAGCACC TCTTGAGGCA TCCCTTGGCT ATTCTGTGCA TATTGTTCTT CAGAGACCTC 1879
ACTACCCACA TGCTGATCTA TTGGGGAACA GAGAAGAGAC AGGCCACTAA GGTACAGGCTC 1939
TTTATATTAA GTTCCCCAGA GGAAGAGTAA GTTGAGAAGG TATCAGTTTA ATGTTGAAGA 1999
ATTGACCTCA GGGCTCAGTT TCCATTCCC TCCCTCAGTA TTCTTCCTGG CAAGATACCC 2059
ATTAAGCATT TCGCCAATCA GAATCTCATT TTATAGTTTT TCCCATTTGGT CTTTAACTAA 2119
GACTTTCTTG TAGCAATCTC GTAAGCAGTG AACCCCTCA GATCAGTAGA ATATAGTATC 2179
TGGGGGAGAA GACTTACTTC CTTCAGGGCA GCAGCCACAG CCAGGCTTCT GTCATACAGG 2239
TAGATCCCCA AGCACAGAGA CATAAAAAG GTCTCCCAGA AAATATAGA CCATTCTCCA 2299
AGTGAATTC CCACTTAGGG CTCTGGTCAC TAGATTGCAA CCTGTGTGTT TGTCATCATC 2359
CTCATCTCAC CATTGTATTG CTATGCCCTC CCATAAAAC ACATTGATCC CTAGCAAGAT 2419



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TATTGCATTC CAGATTTTAC TGCCTTTTGCT AGGCTTTTGC TTAGCAAAGG GCTGACTTTC 2479
CATTGTTATC ATGGTGTATA TATTTTGTGTC ACCATTCCCA CAAGTATACT TGATGTTGTC 2539
ATAGAACGAA CATCCTACTC TATGATTTAC TAACCAATTA CTTTCCCAGA TCATAGACCT 2599
CTCTGCATAG TAGTCATAGG TCTTGACTTT GGGGAAAGAA AAGGAAGCTG CAGGAATATT 2659
TATCTCCAAA GTCGAATGAG AAAGAACTCC AGCAAATCCA ATGGCTACAA ACTAAAAATC 2719
AGCATTATTT CATATTGCTG TTTCTTAGCT GAATATGGAA TAAAGAACTA TTATTTTATT 2779
TTGAAAAAAA AAAAAAAA 2797

FIG. 6H



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CGCGCGCGCGT TTTCCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC 60
TCATACAGAC AAGATCATT TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTG 120
AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTTCAGA AGGAAAGAAA AAATTGCCTC 180
TGCAGGTGTG CGAGCAGGAT TGCTTCTGCA ACAAAGCCT CCACCCAGCC ACATCTTGGG 240
AAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
1 5 10
TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
15 20 25 30
GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
35 40 45
ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
50 55 60
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CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA	480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu	
	65 70 75
GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA	528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val	
	80 85 90
GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG	576
Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val	
	95 100 105 110
GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC	624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val	
	115 120 125
CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG	672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys	
	130 135 140
GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG	720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu	
	145 150 155



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GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA	768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile	
160 165 170	
TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC	816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His	
175 180 185 190	
AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA	864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln	
195 200 205	
ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG	912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg	
210 215 220	
GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT	960
Gly Tyr Leu Thr Ser Phe Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr	
225 230 235	
ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	



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CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT Leu Gly Ala Leu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser 255 260 265 270	1056
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val 275 280 285	1104
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro 290 295 300	1152
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA Cys Tyr Ala Glu Val Leu Arg Val Arg Gly Lys Leu His Gln Pro 305 310 315	1200
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Asp 320 325 330	1248
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Ile Leu 335 340 345 350	1296

FIG. 7D



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AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG 1344
Lys Val Glu Asp Phe 355
360
365
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC 1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr
370
375
380
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC 1440
Ile Thr Ala Leu Lys Asp Gly Phe 390
385
395
TTA CAG CTC ACA AAG AAA GTG AAC ATA GAG ACG GGC TGG GCC TTG 1488
Leu Gln Leu Thr Lys Val Asn Ile Glu Thr Gly Trp Ala Leu
400
405
410
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT 1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
415
420
425
TGAGGCCACG TACTTCCTTG GAGACCTGCA TTGCCAACA CCTTTTAAG GGGAGGAGAG 1590

FIG. 7E



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AGCACTTAGT TTCTGAACTA GTCTGGGACA TCCTGGACTT GAGCCTAGAG ATTAGGTTT 1650
AATTAATTTT ACACATCTAA TGTGAACTGC TGCCTAACCA CTCAAGAGTA CACAGCTGGC 1710
ACCAGAGCAT CACAGAGAGC CCTGTGAGCC AAAAAGTATA GTTTTGGAAAC TTAACCTTGG 1770
AGTGAGAGCC CAGGGACAGG TCCCTGGAAA CCAAAGAAAA ATCGCATTC AACCCTTTGA 1830
GTGCCTCATT CCACTGAATA TTTAAATTTT CCTCTTAAAT GGTAAACTGA CTTATTGCAA 1890
TCCCAAGACC CATCAATATC AGTATTTTTT TCCTCCCCTAT ACAGTGCCCT GCCCACCCTT 1950
ATCTGCACCC ACCTCCCCTG AAAAAGAGAG AAAAAAAAAA AAAAAAAA 1998

FIG. 7F



CD39L2	1	MKGI RYETSRKTSYIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI	
CD39L4	1	-----	
CD39L1	1	-----MATSNG	
CD39L3	1	-----	
CD39	1	-----MFTVLTRQPCEQAGL	
		-----MEDTKE	
ACR I			
CD39L2	61	KWHRATAQAFFSITRAAPGARWGQQAHSPLGTAADGHEVFYGYMF	DAGSTGTRVHVFO
CD39L4	7	TVFFMLVVSVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGYMF	DAGSTGTRI HVYT
CD39L1	1	---MAGKVRSLPPLLAAAGLAGLLLCVPTRDVREP ² ALKYGIVL	DAGSSHTSMFIYK
CD39L3	16	KALYRTPTIIALVLLVLSIVLVSTITVIQHKQEVLPGLKYGIVL	DAGSSRTTVVYQ
CD39	7	SNVKTFCSKNILAILGFSIIAIVIALAVGLTQNKALPENVKYGIVL	DAGSSHTSLYIYK
ACR II			
CD39L2	120	FT-RPPRETPTLTHETFKAVK-PGLSAYADDVEKSAQGI ² RELLDVAKQDIPDFWKA ² PL	
CD39L4	67	FVQKMPGQLPILEGEVFD ² SVK-PGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHWK ² TPV	
CD39L1	58	WPADKENDTGIVGQHSSCDVPGGGISSYADNPSGASQSLVGCLEQALQDVPKERHAG ² PL	
CD39L3	75	WPAEKENNTGVVSQTFKCSVKSGSGISSYGNPNPQDVPRAFE ² ECMKQKVGVPSHLHG ² STPI	
CD39	67	WPAEKENDTGVVHQVEECRVKGP ² GISKEFVQKVNEIGIYLTDCMERAREVIPRSQH ² OETPV	

FIG. 8A



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ACR II		ACR III	
CD39L2	178.	VLKATAGLRLL--PGEKAQKLLQKVKEVFKASPFLVGDDCVSIMN	GTDEGVSAWITINF
CD39L4	126	VLKATAGLRLL--PEHKAKALLFEVKEIFRKSPFLVPKGSVIMDGS	DEGILAWVTVNF
CD39L1	118	YLGATAGMRLLNLTNPEASTSVLMAVTHLTQYPP--DFRGARILSGQEEGVFGWVTANY	
CD39L3	135	HLGATAGMRLLRLQNETAANEVLESIQSYFKSQPF--DFRGAQIIISGQEEGVYGMITANY	
CD39	127	YLGATAGMRLLLRMESEELADRVLDVVERSLSNYPP--DFQGARIIITGQEEGAYGWITINY	
		ACR IV	
CD39L2	235	LTGSL-----KTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRM	
CD39L4	183	LTGQL-----HGRQETVGTLDLGGASTQITFLPQFEKTLQTPRGYLTFSFM	
CD39L1	176	LLENFIKYGVVGRWF--RPR-KGTLGAMDLLGGASTQITFETTSPAEDRASE--V-QLHL	
CD39L3	193	LMGNFLEKNLWHMWV--HPHGVEETGALDLGGASTQISFVAGEKMDLNTSD--IMQVSL	
CD39	185	LLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDN--ALQFRL	
CD39L2	283	FNRTYKLYSYLGLGLMSARLAILGGVEGQPAKDGEKLVSPCLSPSPFKGEWEHAEVTYR	
CD39L4	231	FNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPRWLEAEWIFCGGVKYQ	
CD39L1	229	YGQHYRVYTHSFCLCYGRDQVLQRL-ASALQ-----THGFHPCWPRGFSTQVLLGDVYQS	
CD39L3	248	YGYVYTYTHSFQCYGRNEAEKKFL-AMLLQNSPTKNHLTNPCYPRDYISFTMGHVFDSD	
CD39	242	YGKDYNVYTHSFCLCYGKDQALWQKL-AKDIQVASNEI-LRDPCHFPGYKKVVNVSDLYKT	

FIG. 8B



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CD39L2	343	VSGQKAAASLHELCAARVSEVLQNRVVRHRT EEVKHVD FYAFSYYYDLAAGVGLIDA EKKGG S
CD39L4	290	YGGNQEGEVGFEP CYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDRAVD TDMI DYEKGGI
CD39L1	283	PCTMAQRPNFNSARVSLSGSSDPHL CRDLVSGLFSFSSC -PF SRCSFNGVFPQPPVAGN
CD39L3	307	LCTVDQRPESYNPNDVIT FEGTGDP SLCKEKVASIF DFKACHDQETCSFDGVYQPKIKGP
CD39	300	PCT--KR FEM TL PFQ QFEIQGIGNYQQCHQSILEL FN TSYC-PYSQCAFNGIFL PP LQGD
CD39L2	403	LVVGD FEIAAKYVCR TLETQ QSSP FCMDLTYVSL LQE -FG FPRSKVLK TRKIDNVE
CD39L4	350	LKVED FERKAREVC DNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ LTKKVN NI E
CD39L1	342	FV-----AFSA FFYTVD FLRTSMGLPVATLQ LEAAAVNC QTWAQ-----
CD39L3	367	FV-----AFAGFY YTASALN SGSF--SLDTFNSSTWN FC SNWSQL PL LLPK FD EVY
CD39	357	FG-----AFSAFY FVMKFL NLTS--EKVSQEKV TEMMKKFCAQ PWEEIKTSYAGV XEKY
CD39L2	462	TSWALGAIFHYIDS LN RQKSPAS*
CD39L4	410	TG WALGATFHL LQSLGISH
CD39L1	384	-----QLLSRGYGF DERAF GGVIFQKKAADTAVG WALGYMLN LTNLIPADPPG
CD39L3	418	ARSYCF SANYIYHLFVNGYKFT EETW PQIHFEKEVGN SSIAWSLGYMLSLTNQI PAESPL
CD39	409	LSEYCF SGTYILSLL QGYHFTAD SWEHIHFIGIK QGS DAGWT LG YMLN LTNMIPAEQP-

FIG. 8C



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CD39L2	485	
CD39L4	429	
CD39L1	432	<u>LR</u> <u>KG</u> <u>TD</u> <u>PF</u> <u>SS</u> <u>VV</u> <u>VL</u> <u>LL</u> <u>LF</u> <u>AS</u> <u>AL</u> <u>LA</u> <u>LV</u> <u>LL</u> <u>LR</u> <u>QV</u> <u>HS</u> <u>AK</u> <u>LP</u> <u>ST</u> <u>I</u> *
CD39L3	478	<u>IR</u> <u>LP</u> <u>IE</u> <u>PP</u> <u>VF</u> <u>VG</u> <u>TL</u> <u>AF</u> <u>FT</u> <u>VA</u> <u>AL</u> <u>LC</u> <u>LA</u> <u>FL</u> <u>AY</u> <u>LC</u> <u>SA</u> <u>TR</u> <u>RR</u> <u>KR</u> <u>HS</u> <u>EH</u> <u>AF</u> <u>DH</u> <u>AV</u> <u>DS</u> <u>D</u> *
CD39	468	<u>LS</u> <u>TP</u> <u>LS</u> <u>HS</u> <u>TY</u> <u>VF</u> <u>LM</u> <u>VL</u> <u>ES</u> <u>LV</u> <u>LF</u> <u>TV</u> <u>AI</u> <u>IG</u> <u>LL</u> <u>IF</u> <u>HK</u> <u>PS</u> <u>YF</u> <u>WK</u> <u>DM</u> <u>V</u> *

FIG. 8D

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peaGDP	1	-----M
potapyrase 1	1	-----MLNQN
CD39L2	1	MKGI RYETSRKTSYIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI
CD39L4	1	-----MATSWG
dNTPase	1	-----MKYEYKLLATDEKPPRRKSSGSPNASSGGNRGPGSL
yGDPase	1	-----KTP
ACRI		
peaGDP	2	ELLIKLITFLFSPAITSSQYLGNNL-LTSRKIFLKQEEISSYAVVFFDAGSTGSRIHVV
potapyrase 6	6	SHFIFIILAI FLVLP LSL LSKNVNAQI-PLRRHLLSHESE--HYAVIFDAGSTGSRVHVF
CD39L2	61	KWHRATATQAFFSITRAAPGARWGQQA-H-SPLGTAADGHEVFFYCGIMFDAGSTGTRVHVF
CD39L4	7	TVFFMLVVSVCVCSAVSHRNQQTWFEI-FLSSMCPINVSASTLYGIMFDAGSTGTRIHHV
dNTPase	37	KISPLCLIIISVILLFVFGFVSENASP-YLARLASKFGYSKVQYAAIIDAGSTGSRVLAY
yGDPase	5	DISILPVNDEPGYLQDSKTEQNYPELADAVKQTSQTCSEEHKYYVIMIIDAGSTGSRVHIY

FIG. 9A



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		ACR II	
peaGDP	61	HFNQNLDLLHIGKGV EY YNKITPGLSSYANNPEQA AKSLIPLLLEQAEDVVPDDLQPKTPV	
potapyrase	63	RFDEKLG L L P I G N N I E Y F M A T E P G L S S Y A E D P K A A N S L E P L L D G A E G V V P Q E L Q S E T P L	
CD39L2	119	QFT - RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGI R E L L D V A K Q D I P P D F W K A T P L	
CD39L4	66	TPVQKMPGQLPILEGEVFDVSVPKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHWKKTTPV	
dNTPase	96	KFNRSFIDNKLVLVEELPKERKPGLSFPADNPAEGAH S I K L L L D E A R A F I P K E H W S S T P L	
YGDPase	65	KFD - - VCTSPPTLLDEKFKDML E P G L S S F D T D S V G A A N S L D P L L K V A M N Y V P I K A R S C T P V	
		ACR III	
peaGDP	121	RLGATAGLRLLLNGDASEKILQSVRDMLSNRSTF - NVQPPDAVSIIDGTQEGSYLWVTNNYA	
potapyrase	123	ELGATAGLRLMLKGDAAEKILQAVRNLVKNQSTF - HSKDQWVTILDGTQEGSYMWA A I N Y L	
CD39L2	178	VLKATAGLRLLPGEKAQKLLQKVKEVFK - ASPF - LVGDDCVSIMNGTDEGVSAWITINFL	
CD39L4	126	VLKATAGLRLLP E H K A K A L L F E V K E I F R - K S P F - L V P K G S V S I M D G S D E G I L A W V T V N F L	
dNTPase	156	VLKATAGLRLLPASKAENILNAVRDLFA - KSEF - SVDMDAVEIMDGTDEGIFSWFTVNNFL	
YGDPase	123	AVKATAGLRLLLGDAKSSKILSAVRDHLEKDYPPFPVVEGDGVSIMGGDEEGVFAWITTNYL	

FIG. 9B



		ACR IV	
peaGDP	180	LGNLGGKKYTK--TVGVILGGGSVQ	MAYAVSKKTAKNAPKVADGDDPYIKKVVLKGI PYD
potapyrase	182	LGNLGGKDYKS--TTATIDLGGGSVQ	MAYAISNEQFAKAPQNE DG-EPYVQQKHLM SKDYN
CD39L2	236	TGSLKTPGGS--SVGMLDLGGGSTQ	IAFLPRVEG-----TLQASPPGYLTALRMFNRTYK
CD39L4	184	TGQLHGHRQE--TVGTLDLGGASTQ	ITFLPQFEK-----TLEQTPRGVLTSPFEMFNSTYK
dNTPase	214	LGRLSKTNQA--AA--LDLGGGSTQ	VTFSPTDPD-----QVPVYDK-YMHEVVTS SKKIN
yGDPase	183	LGNIGANGPKLP TAAVFDLGGGSTQ	IVFEPTFPINEXMV-----DGEHKFDLKF G DENYT
		↓	
peaGDP	238	LYVHSYLFHFGREASRAEILKLT PRSP	-----NPCLLAGFNG-----IY
potapyrase	239	LYVHSYLYNQQLAGRAEIFKASRNES	-----NPCALEGCDG-----YY
CD39L2	289	LYSYSYLGLGLMSARLAILGGVEGQPAKD GKELV	-----SPCLSPSPFKG-----E-W
CD39L4	237	LYTHSYLGFGLKAARLATLGALETE-GTDGHTFR	-----SACLPRWLEA-----E-W
dNTPase	264	VFTHSYLGGLGLMAARHAFV--THGYKKEDTVLE	-----SVCVNPIIAN-----RTW
yGDPase	238	LYQFSHLGYGLKEGRNKVNSVLVENALKDGKILKGDNTKT HQLS SPCLPPKVNATNEKVT	

FIG. 9C



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peaGDP	276	<u>T</u> <u>Y</u> <u>S</u> <u>G</u> <u>E</u> <u>E</u> <u>F</u> <u>K</u> <u>A</u> <u>T</u> <u>A</u> <u>Y</u> <u>T</u> <u>S</u> <u>G</u> <u>-</u> <u>A</u> <u>N</u> <u>F</u> <u>N</u> <u>K</u> <u>C</u> <u>K</u> <u>N</u> <u>T</u> <u>I</u> <u>R</u> <u>K</u> <u>A</u> <u>L</u> <u>K</u> <u>L</u> <u>N</u> <u>Y</u> <u>P</u> <u>C</u> <u>P</u> <u>Y</u> <u>O</u> <u>N</u> <u>C</u> <u>T</u> <u>F</u> <u>G</u> <u>G</u> <u>I</u> <u>W</u> <u>N</u> <u>G</u> <u>G</u> <u>-</u> <u>-</u> <u>-</u> <u>G</u> <u>G</u> <u>N</u> <u>G</u> <u>O</u> <u>K</u> <u>N</u>
potapyrase	277	<u>S</u> <u>Y</u> <u>G</u> <u>G</u> <u>V</u> <u>D</u> <u>Y</u> <u>K</u> <u>V</u> <u>K</u> <u>A</u> <u>P</u> <u>K</u> <u>K</u> <u>G</u> <u>-</u> <u>S</u> <u>S</u> <u>W</u> <u>K</u> <u>R</u> <u>C</u> <u>R</u> <u>R</u> <u>L</u> <u>T</u> <u>R</u> <u>H</u> <u>A</u> <u>L</u> <u>K</u> <u>I</u> <u>N</u> <u>A</u> <u>K</u> <u>N</u> <u>I</u> <u>E</u> <u>E</u> <u>C</u> <u>T</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>W</u> <u>N</u> <u>G</u> <u>G</u> <u>-</u> <u>-</u> <u>-</u> <u>G</u> <u>G</u> <u>D</u> <u>G</u> <u>O</u> <u>K</u> <u>N</u>
CD39L2	335	<u>E</u> <u>H</u> <u>A</u> <u>E</u> <u>V</u> <u>T</u> <u>Y</u> <u>R</u> <u>V</u> <u>S</u> <u>G</u> <u>O</u> <u>K</u> <u>A</u> <u>A</u> <u>S</u> <u>L</u> <u>H</u> <u>E</u> <u>L</u> <u>C</u> <u>A</u> <u>A</u> <u>R</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>S</u> <u>E</u> <u>V</u> <u>-</u> <u>-</u> <u>-</u> <u>L</u> <u>Q</u> <u>N</u> <u>R</u> <u>V</u> <u>-</u> <u>-</u> <u>-</u> <u>H</u> <u>R</u> <u>T</u> <u>-</u> <u>-</u> <u>-</u> <u>E</u> <u>E</u> <u>V</u> <u>K</u> <u>H</u> <u>V</u> <u>D</u>
CD39L4	282	<u>I</u> <u>F</u> <u>G</u> <u>G</u> <u>V</u> <u>K</u> <u>Y</u> <u>Q</u> <u>Y</u> <u>G</u> <u>N</u> <u>Q</u> <u>E</u> <u>G</u> <u>E</u> <u>V</u> <u>G</u> <u>F</u> <u>E</u> <u>P</u> <u>C</u> <u>Y</u> <u>A</u> <u>E</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>L</u> <u>R</u> <u>V</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>R</u> <u>G</u> <u>K</u> <u>L</u> <u>-</u> <u>-</u> <u>-</u> <u>H</u> <u>Q</u> <u>P</u> <u>-</u> <u>-</u> <u>-</u> <u>E</u> <u>E</u> <u>V</u> <u>Q</u> <u>R</u> <u>G</u> <u>S</u>
dNTPase	308	<u>T</u> <u>Y</u> <u>G</u> <u>N</u> <u>V</u> <u>Q</u> <u>Y</u> <u>K</u> <u>V</u> <u>S</u> <u>G</u> <u>K</u> <u>E</u> <u>N</u> <u>G</u> <u>K</u> <u>S</u> <u>S</u> <u>A</u> <u>E</u> <u>Q</u> <u>P</u> <u>I</u> <u>V</u> <u>D</u> <u>F</u> <u>D</u> <u>A</u> <u>C</u> <u>L</u> <u>E</u> <u>L</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>K</u> <u>S</u> <u>K</u> <u>V</u> <u>M</u> <u>P</u> <u>L</u> <u>V</u> <u>K</u> <u>P</u> <u>K</u> <u>P</u> <u>-</u> <u>-</u> <u>-</u> <u>F</u> <u>T</u> <u>L</u> <u>K</u> <u>Q</u> <u>H</u> <u>A</u>
YGD Pase	298	<u>L</u> <u>E</u> <u>S</u> <u>K</u> <u>E</u> <u>T</u> <u>Y</u> <u>T</u> <u>I</u> <u>D</u> <u>F</u> <u>I</u> <u>G</u> <u>P</u> <u>D</u> <u>E</u> <u>P</u> <u>S</u> <u>G</u> <u>A</u> <u>Q</u> <u>C</u> <u>R</u> <u>F</u> <u>L</u> <u>T</u> <u>D</u> <u>E</u> <u>I</u> <u>L</u> <u>N</u> <u>K</u> <u>D</u> <u>A</u> <u>Q</u> <u>C</u> <u>S</u> <u>P</u> <u>P</u> <u>C</u> <u>S</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>H</u> <u>Q</u> <u>P</u> <u>S</u> <u>L</u> <u>V</u> <u>R</u> <u>T</u> <u>F</u> <u>K</u> <u>E</u> <u>S</u> <u>N</u> <u>D</u>
peaGDP	332	<u>L</u> <u>P</u> <u>A</u> <u>S</u> <u>S</u> <u>S</u> <u>F</u> <u>F</u> <u>Y</u> <u>L</u> <u>P</u> <u>E</u> <u>D</u> <u>T</u> <u>G</u> <u>M</u> <u>V</u> <u>D</u> <u>A</u> <u>S</u> <u>T</u> <u>P</u> <u>N</u> <u>F</u> <u>I</u> <u>L</u> <u>R</u> <u>P</u> <u>V</u> <u>D</u> <u>I</u> <u>E</u> <u>T</u> <u>K</u> <u>A</u> <u>K</u> <u>E</u> <u>A</u> <u>C</u> <u>A</u> <u>L</u> <u>N</u> <u>F</u> <u>E</u> <u>D</u> <u>A</u> <u>K</u> <u>S</u> <u>T</u> <u>Y</u> <u>P</u> <u>F</u> <u>L</u> <u>D</u> <u>K</u> <u>K</u> <u>N</u> <u>V</u> <u>A</u> <u>S</u>
potapyrase	333	<u>I</u> <u>H</u> <u>A</u> <u>S</u> <u>S</u> <u>F</u> <u>F</u> <u>Y</u> <u>D</u> <u>I</u> <u>G</u> <u>A</u> <u>Q</u> <u>V</u> <u>G</u> <u>I</u> <u>V</u> <u>D</u> <u>T</u> <u>K</u> <u>F</u> <u>P</u> <u>S</u> <u>A</u> <u>L</u> <u>A</u> <u>K</u> <u>P</u> <u>I</u> <u>Q</u> <u>Y</u> <u>L</u> <u>N</u> <u>A</u> <u>A</u> <u>K</u> <u>V</u> <u>A</u> <u>C</u> <u>T</u> <u>N</u> <u>V</u> <u>A</u> <u>D</u> <u>I</u> <u>K</u> <u>S</u> <u>I</u> <u>F</u> <u>P</u> <u>K</u> <u>T</u> <u>Q</u> <u>D</u> <u>R</u> <u>N</u> <u>I</u> <u>-</u> <u>P</u>
CD39L2	379	<u>F</u> <u>Y</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>D</u> <u>L</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>G</u> <u>L</u> <u>I</u> <u>D</u> <u>A</u> <u>E</u> <u>-</u> <u>K</u> <u>G</u> <u>G</u> <u>S</u> <u>L</u> <u>V</u> <u>G</u> <u>D</u> <u>F</u> <u>E</u> <u>I</u> <u>A</u> <u>A</u> <u>K</u> <u>Y</u> <u>V</u> <u>C</u> <u>R</u> <u>T</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>L</u> <u>E</u> <u>T</u> <u>Q</u> <u>P</u> <u>Q</u> <u>S</u> <u>S</u> <u>P</u>
CD39L4	326	<u>F</u> <u>Y</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>D</u> <u>R</u> <u>A</u> <u>V</u> <u>D</u> <u>T</u> <u>M</u> <u>I</u> <u>D</u> <u>Y</u> <u>E</u> <u>-</u> <u>K</u> <u>G</u> <u>G</u> <u>I</u> <u>L</u> <u>K</u> <u>V</u> <u>E</u> <u>D</u> <u>F</u> <u>E</u> <u>R</u> <u>K</u> <u>A</u> <u>R</u> <u>E</u> <u>V</u> <u>C</u> <u>D</u> <u>N</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>L</u> <u>E</u> <u>N</u> <u>F</u> <u>T</u> <u>S</u> <u>G</u> <u>S</u> <u>P</u>
dNTPase	360	<u>V</u> <u>A</u> <u>A</u> <u>F</u> <u>S</u> <u>Y</u> <u>Y</u> <u>F</u> <u>E</u> <u>R</u> <u>A</u> <u>I</u> <u>E</u> <u>S</u> <u>G</u> <u>L</u> <u>V</u> <u>D</u> <u>P</u> <u>L</u> <u>-</u> <u>A</u> <u>G</u> <u>G</u> <u>E</u> <u>T</u> <u>T</u> <u>V</u> <u>E</u> <u>A</u> <u>Y</u> <u>R</u> <u>K</u> <u>K</u> <u>A</u> <u>Q</u> <u>E</u> <u>I</u> <u>C</u> <u>A</u> <u>I</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>P</u> <u>N</u> <u>D</u> <u>E</u> <u>-</u> <u>-</u> <u>-</u> <u>Q</u> <u>P</u>
YGD Pase	358	<u>I</u> <u>Y</u> <u>I</u> <u>F</u> <u>S</u> <u>Y</u> <u>F</u> <u>Y</u> <u>D</u> <u>R</u> <u>T</u> <u>R</u> <u>P</u> <u>L</u> <u>G</u> <u>M</u> <u>P</u> <u>L</u> <u>S</u> <u>F</u> <u>T</u> <u>L</u> <u>N</u> <u>E</u> <u>L</u> <u>N</u> <u>D</u> <u>L</u> <u>A</u> <u>R</u> <u>I</u> <u>V</u> <u>C</u> <u>K</u> <u>G</u> <u>E</u> <u>E</u> <u>T</u> <u>W</u> <u>N</u> <u>S</u> <u>V</u> <u>F</u> <u>S</u> <u>G</u> <u>I</u> <u>A</u> <u>G</u> <u>S</u> <u>L</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>-</u> <u>D</u> <u>E</u> <u>L</u> <u>E</u> <u>S</u> <u>D</u> <u>S</u>

FIG. 9D



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

Applicants: Chadwick et al.

Docket No. 28110/36120B

46/46

peaGDP	392	<u>YVCMDLIYQYVLLVDGFGGLDPLQKITS</u> <u>GKEIEYQDAIVEAAWPLGN</u> <u>AVEAISA</u> <u>LPKFERL</u>
potapyrase	392	<u>YLCMDLIYETLLVDGFGGLNPHKEITVI</u> <u>HDVQYKNYL</u> <u>VGAAPLGCAID</u> <u>LVSS</u> <u>TTNKIRV</u>
CD39L2	428	<u>FSCMDLTYVSL</u> <u>LLQE</u> <u>-FGFPRSKVL</u> <u>KLTRKIDN</u> <u>-----VETSWALGAI</u> <u>FHYIDSLNR</u> <u>QKSP</u>
CD39L4	375	<u>FLCMDLSYITALLKDGFGFADSTVL</u> <u>QLTKKVN</u> <u>-----IETG</u> <u>WALGATFHLLQ</u> <u>SLGISH</u>
dNTPase	406	<u>FMCFDLTFISTLLREGFGLNDG</u> <u>KKIKLYKKIDG</u> <u>-----HEIS</u> <u>WALGCAYNV</u> <u>LTSEKFSNS</u>
YGD Pase	415	<u>HFCLDLSEFQVSL</u> <u>LHTGYDIP</u> <u>LQRELRTG</u> <u>KKIANK</u> <u>-----EIGW</u> <u>CLGASLPL</u> <u>LKADNNW</u> <u>KCKI</u>

peaGDP	452	<u>MYFV</u>
potapyrase	452	<u>ASS*</u>
CD39L2	483	<u>AS*</u>
CD39L4	429	
dNTPase	462	
YGD Pase	471	<u>QSA</u>

FIG. 9E